



Sequence Listing

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Presta, Leonard G.  
Shelton, David L.  
Urfer, Roman

(ii) TITLE OF INVENTION: Human trk Receptors and Neurotrophic Factor Inhibitors

(iii) NUMBER OF SEQUENCES: 41

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Knobbe, Martens, Olson & Bear  
(B) STREET: 620 Newport Center Drive 16th Floor  
(C) CITY: Newport Beach  
(D) STATE: California  
(E) COUNTRY: USA  
(F) ZIP: 92660

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: WinPatin (Genentech)

(vi) CURRENT APPLICATION DATA

(A) APPLICATION NUMBER: 09/724,524  
(B) FILING DATE: 27-NOV-2000  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 09/156,923  
(B) FILING DATE: 18-SEP-1998  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/359,705  
(B) FILING DATE: 20-DEC-1994  
(C) CLASSIFICATION:

(viii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/286846  
(B) FILING DATE: 10-AUG-1994

(viii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/215139  
(B) FILING DATE: 18-MAR-1994

(ix) ATTORNEY/AGENT INFORMATION:

(A) NAME: Dreger, Ginger  
(B) REGISTRATION NUMBER: 33,055  
(C) REFERENCE/DOCKET NUMBER: GENENT.33CP2C2

(x) TELECOMMUNICATION INFORMATION:  
    (A) TELEPHONE: 949/760-0404  
    (B) TELEFAX: 949/760-9502  
(2) INFORMATION FOR SEQ ID NO:1:

    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 3194 base pairs  
        (B) TYPE: Nucleic Acid  
        (C) STRANDEDNESS: Single  
        (D) TOPOLOGY: Linear  
    (ii) MOLECULE TYPE: nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGAAGGTTTA AAGAAGAAGC CGCAAAGCGC AGGGAAGGCC TCCCGGCACG 50  
GGTGGGGGAA AGCGGCCGGT GCAGCGCGGG GACAGGCACT CGGGCTGGCA 100  
CTGGCTGCTA GGGATGTCGT CCTGGATAAG GTGGCATGGA CCCGCCATGG 150  
CGCGGCTCTG GGGCTTCTGC TGGCTGGTTG TGGGCTTCTG GAGGGCCGCT 200  
TTCGCCTGTC CCACGTCCTG CAAATGCAGT GCCTCTCGGA TCTGGTGCAG 250  
CGACCCTTCT CCTGGCATCG TGGCATTTCG GAGATTGGAG CCTAACAGTG 300  
TAGATCCTGA GAACATCACC GAAATTTTCA TCGCAAACCA GAAAAGGTTA 350  
GAAATCATCA ACGAAGATGA TGTGAAGCT TATGTGGGAC TGAGAAATCT 400  
GACAATTGTG GATTCTGGAT TAAAATTTGT GGCTCATAAA GCATTTCTGA 450  
AAAACAGCAA CCTGCAGCAC ATCAATTTTA CCCGAAACAA ACTGACGAGT 500  
TTGTCTAGGA AACATTTCCG TCACCTTGAC TTGTCTGAAC TGATCCTGGT 550  
GGGCAATCCA TTTACATGCT CCTGTGACAT TATGTGGATC AAGACTCTCC 600  
AAGAGGCTAA ATCCAGTCCA GACACTCAGG ATTTGTACTG CCTGAATGAA 650  
AGCAGCAAGA ATATCCCCTT GGCAAACCTG CAGATACCCA ATTGTGGTTT 700  
GCCATCTGCA AATCTGGCCG CACCTAACCT CACTGTGGAG GAAGGAAAGT 750  
CTATCACATT ATCCTGTAGT GTGGCAGGTG ATCCGGTTCC TAATATGTAT 800  
TGGGATGTTG GTAACCTGGT TTCCAAACAT ATGAATGAAA CAAGCCACAC 850  
ACAGGGCTCC TTAAGGATAA CTAACATTTT ATCCGATGAC AGTGGGAAGC 900  
AGATCTCTTG TGTGGCGGAA AATCTTGTA GAGAAGATCA AGATTCTGTC 950  
AACCTCACTG TGCATTTTGC ACCAACTATC ACATTTCTCG AATCTCCAAC 1000  
CTCAGACCAC CACTGGTGCA TTCCATTAC TGTGAAAGGC AACCCAAAAC 1050

CAGCGCTTCA GTGGTTCTAT AACGGGGCAA TATTGAATGA GTCCAAATAC 1100  
 ATCTGTACTA AAATACATGT TACCAATCAC ACGGAGTACC ACGGCTGCCT 1150  
 CCAGCTGGAT AATCCCCTC ACATGAACAA TGGGGACTAC ACTCTAATAG 1200  
 CCAAGAATGA GTATGGGAAG GATGAGAAAC AGATTTCTGC TCACTTCATG 1250  
 GGCTGGCCTG GAATTGACGA TGGTGCAAAC CCAAATTATC CTGATGTAAT 1300  
 TTATGAAGAT TATGGAAGTG CAGCGAATGA CATCGGGGAC ACCACGAACA 1350  
 GAAGTAATGA AATCCCTTCC ACAGACGTCA CTGATAAAAC CGGTCGGGAA 1400  
 CATCTCTCGG TCTATGCTGT GGTGGTGATT GCGTCTGTGG TGGGATTTTG 1450  
 CCTTTTGGTA ATGCTGTTTC TGCTTAAGTT GGCAAGACAC TCCAAGTTTG 1500  
 GCATGAAAGG CCCAGCCTCC GTTATCAGCA ATGATGATGA CTCTGCCAGC 1550  
 CCACTCCATC ACATCTCCAA TGGGAGTAAC ACTCCATCTT CTTCCGAAGG 1600  
 TGGCCCAGAT GCTGTCATTA TTGGAATGAC CAAGATCCCT GTCATTGAAA 1650  
 ATCCCCAGTA CTTTGGCATC ACCAACAGTC AGCTCAAGCC AGACACATTT 1700  
 GTTCAGCACA TCAAGCGACA TAACATTGTT CTGAAAAGGG AGCTAGGCGA 1750  
 AGGAGCCTTT GGAAAAGTGT TCCTAGCTGA ATGCTATAAC CTCTGTCCTG 1800  
 AGCAGGACAA GATCTTGGTG GCAGTGAAGA CCCTGAAGGA TGCCAGTGAC 1850  
 AATGCACGCA AGGACTTCCA CCGTGAGGCC GAGCTCCTGA CCAACCTCCA 1900  
 GCATGAGCAC ATCGTCAAGT TCTATGGCGT CTGCGTGGAG GGCGACCCCC 1950  
 TCATCATGGT CTTTGAGTAC ATGAAGCATG GGGACCTCAA CAAGTTCCTC 2000  
 AGGGCACACG GCCCTGATGC CGTGCTGATG GCTGAGGGCA ACCCGCCAC 2050  
 GGAAGTACG CAGTCGAGA TGCTGCATAT AGCCCAGCAG ATCGCCGCGG 2100  
 GCATGGTCTA CCTGGCGTCC CAGCACTTCG TGCACCGCGA TTTGGCCACC 2150  
 AGGAACTGCC TGGTCGGGGA GAACTTGCTG GTGAAAATCG GGGACTTTGG 2200  
 GATGTCCCGG GACGTGTACA GCACTGACTA CTACAGGGTC GGTGGCCACA 2250  
 CAATGCTGCC CATTGCTGG ATGCCTCCAG AGAGCATCAT GTACAGGAAA 2300  
 TTCACGACGG AAAGCGACGT CTGGAGCCTG GGGGTCGTGT TGTGGGAGAT 2350  
 TTTCACCTAT GGCAAACAGC CCTGGTACCA GCTGTCAAAC AATGAGGTGA 2400  
 TAGAGTGTAT CACTCAGGGC CGAGTCCTGC AGCGACCCCG CACGTGCCCC 2450  
 CAGGAGGTGT ATGAGCTGAT GCTGGGGTGC TGGCAGCGAG AGCCCCACAT 2500

GAGGAAGAAC ATCAAGGGCA TCCATACCCT CCTTCAGAAC TTGGCCAAGG 2550  
CATCTCCGGT CTACCTGGAC ATTCTAGGCT AGGGCCCTTT TCCCCAGACC 2600  
GATCCTTCCC AACGTACTCC TCAGACGGGC TGAGAGGATG AACATCTTTT 2650  
AACTGCCGCT GGAGGCCACC AAGCTGCTCT CCTTCACTCT GACAGTATTA 2700  
ACATCAAAGA CTCCGAGAAG CTCTCGAGGG AAGCAGTGTG TACTTCTTCA 2750  
TCCATAGACA CAGTATTGAC TTCTTTTTTG CATTATCTCT TTCTCTCTTT 2800  
CCATCTCCCT TGGTTGTTCC TTTTCTTTT TTTAAATTTT CTTTTTCTTC 2850  
TTTTTTTTTCG TCTTCCCTGC TTCACGATTC TTACCCTTTC TTTTGAATCA 2900  
ATCTGGCTTC TGCATTACTA TTAAGTCTGC ATAGACAAAG GCCTTAACAA 2950  
ACGTAATTTG TTATATCAGC AGACACTCCA GTTTGCCAC CACAACAAAC 3000  
AATGCCCTGT TGTATTCCTG CCTTTGATGT GGATGAAAAA AAGGGAAAAC 3050  
AAATATTTCA CTTAACTTT GTCACCTCTG CTGTACAGAT ATCGAGAGTT 3100  
TCTATGGATT CACTTCTATT TATTTATTAT TATTACTGTT CTTATTGTTT 3150  
TTGGATGGCT TAAGCCTGTG TATAAAAAA AAAAAAATC TAGA 3194

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Ser	Ser	Trp	Ile	Arg	Trp	His	Gly	Pro	Ala	Met	Ala	Arg	Leu
1				5				10						15
Trp	Gly	Phe	Cys	Trp	Leu	Val	Val	Gly	Phe	Trp	Arg	Ala	Ala	Phe
			20					25						30
Ala	Cys	Pro	Thr	Ser	Cys	Lys	Cys	Ser	Ala	Ser	Arg	Ile	Trp	Cys
			35					40						45
Ser	Asp	Pro	Ser	Pro	Gly	Ile	Val	Ala	Phe	Pro	Arg	Leu	Glu	Pro
			50					55						60
Asn	Ser	Val	Asp	Pro	Glu	Asn	Ile	Thr	Glu	Ile	Phe	Ile	Ala	Asn
			65					70						75
Gln	Lys	Arg	Leu	Glu	Ile	Ile	Asn	Glu	Asp	Asp	Val	Glu	Ala	Tyr
			80					85						90
Val	Gly	Leu	Arg	Asn	Leu	Thr	Ile	Val	Asp	Ser	Gly	Leu	Lys	Phe

				95					100					105
Val	Ala	His	Lys	Ala 110	Phe	Leu	Lys	Asn	Ser 115	Asn	Leu	Gln	His	Ile 120
Asn	Phe	Thr	Arg	Asn 125	Lys	Leu	Thr	Ser	Leu 130	Ser	Arg	Lys	His	Phe 135
Arg	His	Leu	Asp	Leu 140	Ser	Glu	Leu	Ile	Leu 145	Val	Gly	Asn	Pro	Phe 150
Thr	Cys	Ser	Cys	Asp 155	Ile	Met	Trp	Ile	Lys 160	Thr	Leu	Gln	Glu	Ala 165
Lys	Ser	Ser	Pro	Asp 170	Thr	Gln	Asp	Leu	Tyr 175	Cys	Leu	Asn	Glu	Ser 180
Ser	Lys	Asn	Ile	Pro 185	Leu	Ala	Asn	Leu	Gln 190	Ile	Pro	Asn	Cys	Gly 195
Leu	Pro	Ser	Ala	Asn 200	Leu	Ala	Ala	Pro	Asn 205	Leu	Thr	Val	Glu	Glu 210
Gly	Lys	Ser	Ile	Thr 215	Leu	Ser	Cys	Ser	Val 220	Ala	Gly	Asp	Pro	Val 225
Pro	Asn	Met	Tyr	Trp 230	Asp	Val	Gly	Asn	Leu 235	Val	Ser	Lys	His	Met 240
Asn	Glu	Thr	Ser	His 245	Thr	Gln	Gly	Ser	Leu 250	Arg	Ile	Thr	Asn	Ile 255
Ser	Ser	Asp	Asp	Ser 260	Gly	Lys	Gln	Ile	Ser 265	Cys	Val	Ala	Glu	Asn 270
Leu	Val	Gly	Glu	Asp 275	Gln	Asp	Ser	Val	Asn 280	Leu	Thr	Val	His	Phe 285
Ala	Pro	Thr	Ile	Thr 290	Phe	Leu	Glu	Ser	Pro 295	Thr	Ser	Asp	His	His 300
Trp	Cys	Ile	Pro	Phe 305	Thr	Val	Lys	Gly	Asn 310	Pro	Lys	Pro	Ala	Leu 315
Gln	Trp	Phe	Tyr	Asn 320	Gly	Ala	Ile	Leu	Asn 325	Glu	Ser	Lys	Tyr	Ile 330
Cys	Thr	Lys	Ile	His 335	Val	Thr	Asn	His	Thr 340	Glu	Tyr	His	Gly	Cys 345
Leu	Gln	Leu	Asp	Asn 350	Pro	Thr	His	Met	Asn 355	Asn	Gly	Asp	Tyr	Thr 360
Leu	Ile	Ala	Lys	Asn 365	Glu	Tyr	Gly	Lys	Asp 370	Glu	Lys	Gln	Ile	Ser 375
Ala	His	Phe	Met	Gly	Trp	Pro	Gly	Ile	Asp	Asp	Gly	Ala	Asn	Pro

				380					385					390
Asn	Tyr	Pro	Asp	Val 395	Ile	Tyr	Glu	Asp	Tyr 400	Gly	Thr	Ala	Ala	Asn 405
Asp	Ile	Gly	Asp	Thr 410	Thr	Asn	Arg	Ser	Asn 415	Glu	Ile	Pro	Ser	Thr 420
Asp	Val	Thr	Asp	Lys 425	Thr	Gly	Arg	Glu	His 430	Leu	Ser	Val	Tyr	Ala 435
Val	Val	Val	Ile	Ala 440	Ser	Val	Val	Gly	Phe 445	Cys	Leu	Leu	Val	Met 450
Leu	Phe	Leu	Leu	Lys 455	Leu	Ala	Arg	His	Ser 460	Lys	Phe	Gly	Met	Lys 465
Gly	Pro	Ala	Ser	Val 470	Ile	Ser	Asn	Asp	Asp 475	Asp	Ser	Ala	Ser	Pro 480
Leu	His	His	Ile	Ser 485	Asn	Gly	Ser	Asn	Thr 490	Pro	Ser	Ser	Ser	Glu 495
Gly	Gly	Pro	Asp	Ala 500	Val	Ile	Ile	Gly	Met 505	Thr	Lys	Ile	Pro	Val 510
Ile	Glu	Asn	Pro	Gln 515	Tyr	Phe	Gly	Ile	Thr 520	Asn	Ser	Gln	Leu	Lys 525
Pro	Asp	Thr	Phe	Val 530	Gln	His	Ile	Lys	Arg 535	His	Asn	Ile	Val	Leu 540
Lys	Arg	Glu	Leu	Gly 545	Glu	Gly	Ala	Phe	Gly 550	Lys	Val	Phe	Leu	Ala 555
Glu	Cys	Tyr	Asn	Leu 560	Cys	Pro	Glu	Gln	Asp 565	Lys	Ile	Leu	Val	Ala 570
Val	Lys	Thr	Leu	Lys 575	Asp	Ala	Ser	Asp	Asn 580	Ala	Arg	Lys	Asp	Phe 585
His	Arg	Glu	Ala	Glu 590	Leu	Leu	Thr	Asn	Leu 595	Gln	His	Glu	His	Ile 600
Val	Lys	Phe	Tyr	Gly 605	Val	Cys	Val	Glu	Gly 610	Asp	Pro	Leu	Ile	Met 615
Val	Phe	Glu	Tyr	Met 620	Lys	His	Gly	Asp	Leu 625	Asn	Lys	Phe	Leu	Arg 630
Ala	His	Gly	Pro	Asp 635	Ala	Val	Leu	Met	Ala 640	Glu	Gly	Asn	Pro	Pro 645
Thr	Glu	Leu	Thr	Gln 650	Ser	Gln	Met	Leu	His 655	Ile	Ala	Gln	Gln	Ile 660
Ala	Ala	Gly	Met	Val	Tyr	Leu	Ala	Ser	Gln	His	Phe	Val	His	Arg

665										670					675				
Asp	Leu	Ala	Thr	Arg	Asn	Cys	Leu	Val	Gly	Glu	Asn	Leu	Leu	Val					
				680					685					690					
Lys	Ile	Gly	Asp	Phe	Gly	Met	Ser	Arg	Asp	Val	Tyr	Ser	Thr	Asp					
				695					700					705					
Tyr	Tyr	Arg	Val	Gly	Gly	His	Thr	Met	Leu	Pro	Ile	Arg	Trp	Met					
				710					715					720					
Pro	Pro	Glu	Ser	Ile	Met	Tyr	Arg	Lys	Phe	Thr	Thr	Glu	Ser	Asp					
				725					730					735					
Val	Trp	Ser	Leu	Gly	Val	Val	Leu	Trp	Glu	Ile	Phe	Thr	Tyr	Gly					
				740					745					750					
Lys	Gln	Pro	Trp	Tyr	Gln	Leu	Ser	Asn	Asn	Glu	Val	Ile	Glu	Cys					
				755					760					765					
Ile	Thr	Gln	Gly	Arg	Val	Leu	Gln	Arg	Pro	Arg	Thr	Cys	Pro	Gln					
				770					775					780					
Glu	Val	Tyr	Glu	Leu	Met	Leu	Gly	Cys	Trp	Gln	Arg	Glu	Pro	His					
				785					790					795					
Met	Arg	Lys	Asn	Ile	Lys	Gly	Ile	His	Thr	Leu	Leu	Gln	Asn	Leu					
				800					805					810					
Ala	Lys	Ala	Ser	Pro	Val	Tyr	Leu	Asp	Ile	Leu	Gly								
				815					820		822								

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1870 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGAAGGTTTA AAGAAGAAGC CGCAAAGCGC AGGGAAGGCC TCCCGGCACG 50

GGTGGGGGAA AGCGGCCGGT GCAGCGCGGG GACAGGCACT CGGGCTGGCA 100

CTGGCTGCTA GGGATGTCGT CCTGGATAAG GTGGCATGGA CCCGCCATGG 150

CGCGGCTCTG GGGCTTCTGC TGGCTGGTTG TGGGCTTCTG GAGGGCCGCT 200

TTCGCCTGTC CCACGTCCTG CAAATGCAGT GCCTCTCGGA TCTGGTGCAG 250

CGACCCTTCT CCTGGCATCG TGGCATTTCG GAGATTGGAG CCTAACAGTG 300

TAGATCCTGA GAACATCACC GAAATTTTCA TCGCAAACCA GAAAAGGTTA 350





TTAATGCTTC TCTTCTTACA GTAGTTCAAA TACAAAAC TG AAATGAAATC 1850

CCATTGGATT GTACTTCTCT 1870

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Ser	Ser	Trp	Ile	Arg	Trp	His	Gly	Pro	Ala	Met	Ala	Arg	Leu	1	5	10	15
Trp	Gly	Phe	Cys	Trp	Leu	Val	Val	Gly	Phe	Trp	Arg	Ala	Ala	Phe	20	25	30	
Ala	Cys	Pro	Thr	Ser	Cys	Lys	Cys	Ser	Ala	Ser	Arg	Ile	Trp	Cys	35	40	45	
Ser	Asp	Pro	Ser	Pro	Gly	Ile	Val	Ala	Phe	Pro	Arg	Leu	Glu	Pro	50	55	60	
Asn	Ser	Val	Asp	Pro	Glu	Asn	Ile	Thr	Glu	Ile	Phe	Ile	Ala	Asn	65	70	75	
Gln	Lys	Arg	Leu	Glu	Ile	Ile	Asn	Glu	Asp	Asp	Val	Glu	Ala	Tyr	80	85	90	
Val	Gly	Leu	Arg	Asn	Leu	Thr	Ile	Val	Asp	Ser	Gly	Leu	Lys	Phe	95	100	105	
Val	Ala	His	Lys	Ala	Phe	Leu	Lys	Asn	Ser	Asn	Leu	Gln	His	Ile	110	115	120	
Asn	Phe	Thr	Arg	Asn	Lys	Leu	Thr	Ser	Leu	Ser	Arg	Lys	His	Phe	125	130	135	
Arg	His	Leu	Asp	Leu	Ser	Glu	Leu	Ile	Leu	Val	Gly	Asn	Pro	Phe	140	145	150	
Thr	Cys	Ser	Cys	Asp	Ile	Met	Trp	Ile	Lys	Thr	Leu	Gln	Glu	Ala	155	160	165	
Lys	Ser	Ser	Pro	Asp	Thr	Gln	Asp	Leu	Tyr	Cys	Leu	Asn	Glu	Ser	170	175	180	
Ser	Lys	Asn	Ile	Pro	Leu	Ala	Asn	Leu	Gln	Ile	Pro	Asn	Cys	Gly	185	190	195	
Leu	Pro	Ser	Ala	Asn	Leu	Ala	Ala	Pro	Asn	Leu	Thr	Val	Glu	Glu	200	205	210	
Gly	Lys	Ser	Ile	Thr	Leu	Ser	Cys	Ser	Val	Ala	Gly	Asp	Pro	Val				

215	220	225
Pro Asn Met Tyr Trp Asp Val Gly Asn	Leu Val Ser Lys His Met	
230	235	240
Asn Glu Thr Ser His Thr Gln Gly Ser	Leu Arg Ile Thr Asn Ile	
245	250	255
Ser Ser Asp Asp Ser Gly Lys Gln Ile	Ser Cys Val Ala Glu Asn	
260	265	270
Leu Val Gly Glu Asp Gln Asp Ser Val	Asn Leu Thr Val His Phe	
275	280	285
Ala Pro Thr Ile Thr Phe Leu Glu Ser	Pro Thr Ser Asp His His	
290	295	300
Trp Cys Ile Pro Phe Thr Val Lys Gly	Asn Pro Lys Pro Ala Leu	
305	310	315
Gln Trp Phe Tyr Asn Gly Ala Ile Leu	Asn Glu Ser Lys Tyr Ile	
320	325	330
Cys Thr Lys Ile His Val Thr Asn His	Thr Glu Tyr His Gly Cys	
335	340	345
Leu Gln Leu Asp Asn Pro Thr His Met	Asn Asn Gly Asp Tyr Thr	
350	355	360
Leu Ile Ala Lys Asn Glu Tyr Gly Lys	Asp Glu Lys Gln Ile Ser	
365	370	375
Ala His Phe Met Gly Trp Pro Gly Ile	Asp Asp Gly Ala Asn Pro	
380	385	390
Asn Tyr Pro Asp Val Ile Tyr Glu Asp	Tyr Gly Thr Ala Ala Asn	
395	400	405
Asp Ile Gly Asp Thr Thr Asn Arg Ser	Asn Glu Ile Pro Ser Thr	
410	415	420
Asp Val Thr Asp Lys Thr Gly Arg Glu	His Leu Ser Val Tyr Ala	
425	430	435
Val Val Val Ile Ala Ser Val Val Gly	Phe Cys Leu Leu Val Met	
440	445	450
Leu Phe Leu Leu Lys Leu Ala Arg His	Ser Lys Phe Gly Met Lys	
455	460	465
Gly Phe Val Leu Phe His Lys Ile Pro	Leu Asp Gly	
470	475	477

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2715 base pairs

(B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GGATCCGCGT CGGAGATGGA TGTCTCTCTT TGCCAGCCA AGTGTAGTTT 50  
 CTGGCGGATT TTCTTGCTGG GAAGCGTCTG GCTGGACTAT GTGGGCTCCG 100  
 TGCTGGCTTG CCCTGCAAAT TGTGTCTGCA GCAAGACTGA GATCAATTGC 150  
 CGGCGGCCGG ACGATGGGAA CCTCTTCCCC CTCCTGGAAG GGCAGGATTC 200  
 AGGGAACAGC AATGGGAACG CCAATATCAA CATCACGGAC ATCTCAAGGA 250  
 ATATCACTTC CATAACATA GAGAACTGGC GCAGTCTTCA CACGCTCAAC 300  
 GCCGTGGACA TGGAGCTCTA CACCGGACTT CAAAAGCTGA CCATCAAGAA 350  
 CTCAGGACTT CGGAGCATTC AGCCAGAGC CTTTGCCAAG AACCCCCATT 400  
 TGC GTTATAT AAACCTGTCA AGTAACCGGC TCACCACACT CTCGTGGCAG 450  
 CTCTTCCAGA CGCTGAGTCT TCGGGAATTG CAGTTGGAGC AGAACTTTTT 500  
 CAACTGCAGC TGTGACATCC GCTGGATGCA GCTCTGGCAG GAGCAGGGGG 550  
 AGGCCAAGCT CAACAGCCAG AACCTCTACT GCATCAATGC TGATGGCTCC 600  
 CAGCTTCCTC TCTTCCGCAT GAACATCAGT CAGTGTGACC TTCCTGAGAT 650  
 CAGCGTGAGC CACGTCAACC TGACCGTACG AGAGGGTGAC AATGCTGTTA 700  
 TCACTTGCAA TGGCTCTGGA TCACCCCTTC CTGATGTGGA CTGGATAGTC 750  
 ACTGGGCTGC AGTCCATCAA CACTCACCAG ACCAATCTGA ACTGGACCAA 800  
 TGTTTCATGCC ATCAACTTGA CGCTGGTGAA TGTGACGAGT GAGGACAATG 850  
 GCTTCACCCT GACGTGCATT GCAGAGAACG TGGTGGGCAT GAGCAATGCC 900  
 AGTGTGCCCC TCACTGTCTA CTATCCCCCA CGTGTGGTGA GCCTGGAGGA 950  
 GCCTGAGCTG CGCCTGGAGC ACTGCATCGA GTTTGTGGTG CGTGGCAACC 1000  
 CCCACCAAC GCTGCACTGG CTGCACAATG GGCAGCCTCT GCGGGAGTCC 1050  
 AAGATCATCC ATGTGGAATA CTACCAAGAG GGAGAGATTT CCGAGGGCTG 1100  
 CCTGCTCTTC AACAAAGCCCA CCCACTACAA CAATGGCAAC TATACCCTCA 1150  
 TTGCCAAAAA CCCACTGGGC ACAGCCAACC AGACCATCAA TGGCCACTTC 1200  
 CTCAAGGAGC CCTTTCCAGA GAGCACGGAT AACTTTATCT TGTTTGACGA 1250

AGTGAGTCCC ACACCTCCTA TCACTGTGAC CCACAAACCA GAAGAAGACA 1300  
 CTTTTGGGGT ATCCATAGCA GTTGGACTTG CTGCTTTTGC CTGTGTCCTG 1350  
 TTGGTGGTTC TCTTCGTCAT GATCAACAAA TATGGTCGAC GGTCCAAATT 1400  
 TGGAATGAAG GGTCCCGTGG CTGTCATCAG TGGTGAGGAG GACTCAGCCA 1450  
 GCCCACTGCA CCACATCAAC CACGGCATCA CCACGCCCTC GTCACTGGAT 1500  
 GCCGGGCCCCG AACTGTGGT CATTGGCATG ACTCGCATCC CTGTCATTGA 1550  
 GAACCCCCAG TACTTCCGTC AGGGACACAA CTGCCACAAG CCGGACACGT 1600  
 ATGTGCAGCA CATTAAGAGG AGAGACATCG TGCTGAAGCG AGAACTGGGT 1650  
 GAGGGAGCCT TTGGAAAGGT CTTCTGGGCC GAGTGCTACA ACCTCAGCCC 1700  
 GACCAAGGAC AAGATGCTTG TGGCTGTGAA GGCCCTGAAG GATCCCACCC 1750  
 TGGCTGCCCCG GAAGGATTTT CAGAGGGAGG CCGAGCTGCT CACCAACCTG 1800  
 CAGCATGAGC ACATTGTCAA GTTCTATGGA GTGTGCGGCG ATGGGGACCC 1850  
 CCTCATCATG GTCTTTGAAT ACATGAAGCA TGGAGACCTG AATAAGTTCC 1900  
 TCAGGGCCCA TGGGCCAGAT GCAATGATCC TTGTGGATGG ACAGCCACGC 1950  
 CAGGCCAAGG GTGAGCTGGG GCTCTCCCAA ATGCTCCACA TTGCCAGTCA 2000  
 GATCGCCTCG GGTATGGTGT ACCTGGCCTC CCAGCACTTT GTGCACCGAG 2050  
 ACCTGGCCAC CAGGAACTGC CTGGTTGGAG CGAATCTGCT AGTGAAGATT 2100  
 GGGGACTTCG GCATGTCCAG AGATGTCTAC AGCACGGATT ATTACAGGCT 2150  
 CTTTAATCCA TCTGGAAATG ATTTTTGTAT ATGGTGTGAG GTGGGAGGAC 2200  
 ACACCATGCT CCCCATTCGC TGGATGCCTC CTGAAAGCAT CATGTACCGG 2250  
 AAGTTCAC TA CAGAGAGTGA TGTATGGAGC TTCGGGGTGA TCCTCTGGGA 2300  
 GATCTTCACC TATGGAAAGC AGCCATGGTT CCAACTCTCA AACACGGAGG 2350  
 TCATTGAGTG CATTACCCAA GGTCGTGTTT TGGAGCGGCC CCGAGTCTGC 2400  
 CCCAAAGAGG TGTACGATGT CATGCTGGGG TGCTGGCAGA GGGAACCACA 2450  
 GCAGCGGTTG AACATCAAGG AGATCTACAA AATCCTCCAT GCTTTGGGGA 2500  
 AGGCCACCCC AATCTACCTG GACATTCTTG GCTAGTGGTG GCTGGTGGTC 2550  
 ATGAATTCAT ACTCTGTTGC CTCCTCTCTC CCTGCCTCAC ATCTCCCTTC 2600  
 CACCTCACAA CTCCTTCCAT CCTTGACTGA AGCGAACATC TTCATATAAA 2650  
 CTCAAGTGCC TGCTACACAT ACAACACTGA AAAAAGGAAA AAAAAAGAAA 2700

AAAAAAAAAA ACCGC 2715

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 839 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Asp	Val	Ser	Leu	Cys	Pro	Ala	Lys	Cys	Ser	Phe	Trp	Arg	Ile	1	5	10	15
Phe	Leu	Leu	Gly	Ser	Val	Trp	Leu	Asp	Tyr	Val	Gly	Ser	Val	Leu	20	25	30	
Ala	Cys	Pro	Ala	Asn	Cys	Val	Cys	Ser	Lys	Thr	Glu	Ile	Asn	Cys	35	40	45	
Arg	Arg	Pro	Asp	Asp	Gly	Asn	Leu	Phe	Pro	Leu	Leu	Glu	Gly	Gln	50	55	60	
Asp	Ser	Gly	Asn	Ser	Asn	Gly	Asn	Ala	Asn	Ile	Asn	Ile	Thr	Asp	65	70	75	
Ile	Ser	Arg	Asn	Ile	Thr	Ser	Ile	His	Ile	Glu	Asn	Trp	Arg	Ser	80	85	90	
Leu	His	Thr	Leu	Asn	Ala	Val	Asp	Met	Glu	Leu	Tyr	Thr	Gly	Leu	95	100	105	
Gln	Lys	Leu	Thr	Ile	Lys	Asn	Ser	Gly	Leu	Arg	Ser	Ile	Gln	Pro	110	115	120	
Arg	Ala	Phe	Ala	Lys	Asn	Pro	His	Leu	Arg	Tyr	Ile	Asn	Leu	Ser	125	130	135	
Ser	Asn	Arg	Leu	Thr	Thr	Leu	Ser	Trp	Gln	Leu	Phe	Gln	Thr	Leu	140	145	150	
Ser	Leu	Arg	Glu	Leu	Gln	Leu	Glu	Gln	Asn	Phe	Phe	Asn	Cys	Ser	155	160	165	
Cys	Asp	Ile	Arg	Trp	Met	Gln	Leu	Trp	Gln	Glu	Gln	Gly	Glu	Ala	170	175	180	
Lys	Leu	Asn	Ser	Gln	Asn	Leu	Tyr	Cys	Ile	Asn	Ala	Asp	Gly	Ser	185	190	195	
Gln	Leu	Pro	Leu	Phe	Arg	Met	Asn	Ile	Ser	Gln	Cys	Asp	Leu	Pro	200	205	210	
Glu	Ile	Ser	Val	Ser	His	Val	Asn	Leu	Thr	Val	Arg	Glu	Gly	Asp	215	220	225	

Asn	Ala	Val	Ile	Thr	Cys	Asn	Gly	Ser	Gly	Ser	Pro	Leu	Pro	Asp	230	235	240
Val	Asp	Trp	Ile	Val	Thr	Gly	Leu	Gln	Ser	Ile	Asn	Thr	His	Gln	245	250	255
Thr	Asn	Leu	Asn	Trp	Thr	Asn	Val	His	Ala	Ile	Asn	Leu	Thr	Leu	260	265	270
Val	Asn	Val	Thr	Ser	Glu	Asp	Asn	Gly	Phe	Thr	Leu	Thr	Cys	Ile	275	280	285
Ala	Glu	Asn	Val	Val	Gly	Met	Ser	Asn	Ala	Ser	Val	Ala	Leu	Thr	290	295	300
Val	Tyr	Tyr	Pro	Pro	Arg	Val	Val	Ser	Leu	Glu	Glu	Pro	Glu	Leu	305	310	315
Arg	Leu	Glu	His	Cys	Ile	Glu	Phe	Val	Val	Arg	Gly	Asn	Pro	Pro	320	325	330
Pro	Thr	Leu	His	Trp	Leu	His	Asn	Gly	Gln	Pro	Leu	Arg	Glu	Ser	335	340	345
Lys	Ile	Ile	His	Val	Glu	Tyr	Tyr	Gln	Glu	Gly	Glu	Ile	Ser	Glu	350	355	360
Gly	Cys	Leu	Leu	Phe	Asn	Lys	Pro	Thr	His	Tyr	Asn	Asn	Gly	Asn	365	370	375
Tyr	Thr	Leu	Ile	Ala	Lys	Asn	Pro	Leu	Gly	Thr	Ala	Asn	Gln	Thr	380	385	390
Ile	Asn	Gly	His	Phe	Leu	Lys	Glu	Pro	Phe	Pro	Glu	Ser	Thr	Asp	395	400	405
Asn	Phe	Ile	Leu	Phe	Asp	Glu	Val	Ser	Pro	Thr	Pro	Pro	Ile	Thr	410	415	420
Val	Thr	His	Lys	Pro	Glu	Glu	Asp	Thr	Phe	Gly	Val	Ser	Ile	Ala	425	430	435
Val	Gly	Leu	Ala	Ala	Phe	Ala	Cys	Val	Leu	Leu	Val	Val	Leu	Phe	440	445	450
Val	Met	Ile	Asn	Lys	Tyr	Gly	Arg	Arg	Ser	Lys	Phe	Gly	Met	Lys	455	460	465
Gly	Pro	Val	Ala	Val	Ile	Ser	Gly	Glu	Glu	Asp	Ser	Ala	Ser	Pro	470	475	480
Leu	His	His	Ile	Asn	His	Gly	Ile	Thr	Thr	Pro	Ser	Ser	Leu	Asp	485	490	495
Ala	Gly	Pro	Asp	Thr	Val	Val	Ile	Gly	Met	Thr	Arg	Ile	Pro	Val	500	505	510

6976464.07464

Ile	Glu	Asn	Pro	Gln	Tyr	Phe	Arg	Gln	Gly	His	Asn	Cys	His	Lys	515	520	525
Pro	Asp	Thr	Tyr	Val	Gln	His	Ile	Lys	Arg	Arg	Asp	Ile	Val	Leu	530	535	540
Lys	Arg	Glu	Leu	Gly	Glu	Gly	Ala	Phe	Gly	Lys	Val	Phe	Leu	Ala	545	550	555
Glu	Cys	Tyr	Asn	Leu	Ser	Pro	Thr	Lys	Asp	Lys	Met	Leu	Val	Ala	560	565	570
Val	Lys	Ala	Leu	Lys	Asp	Pro	Thr	Leu	Ala	Ala	Arg	Lys	Asp	Phe	575	580	585
Gln	Arg	Glu	Ala	Glu	Leu	Leu	Thr	Asn	Leu	Gln	His	Glu	His	Ile	590	595	600
Val	Lys	Phe	Tyr	Gly	Val	Cys	Gly	Asp	Gly	Asp	Pro	Leu	Ile	Met	605	610	615
Val	Phe	Glu	Tyr	Met	Lys	His	Gly	Asp	Leu	Asn	Lys	Phe	Leu	Arg	620	625	630
Ala	His	Gly	Pro	Asp	Ala	Met	Ile	Leu	Val	Asp	Gly	Gln	Pro	Arg	635	640	645
Gln	Ala	Lys	Gly	Glu	Leu	Gly	Leu	Ser	Gln	Met	Leu	His	Ile	Ala	650	655	660
Ser	Gln	Ile	Ala	Ser	Gly	Met	Val	Tyr	Leu	Ala	Ser	Gln	His	Phe	665	670	675
Val	His	Arg	Asp	Leu	Ala	Thr	Arg	Asn	Cys	Leu	Val	Gly	Ala	Asn	680	685	690
Leu	Leu	Val	Lys	Ile	Gly	Asp	Phe	Gly	Met	Ser	Arg	Asp	Val	Tyr	695	700	705
Ser	Thr	Asp	Tyr	Tyr	Arg	Leu	Phe	Asn	Pro	Ser	Gly	Asn	Asp	Phe	710	715	720
Cys	Ile	Trp	Cys	Glu	Val	Gly	Gly	His	Thr	Met	Leu	Pro	Ile	Arg	725	730	735
Trp	Met	Pro	Pro	Glu	Ser	Ile	Met	Tyr	Arg	Lys	Phe	Thr	Thr	Glu	740	745	750
Ser	Asp	Val	Trp	Ser	Phe	Gly	Val	Ile	Leu	Trp	Glu	Ile	Phe	Thr	755	760	765
Tyr	Gly	Lys	Gln	Pro	Trp	Phe	Gln	Leu	Ser	Asn	Thr	Glu	Val	Ile	770	775	780
Glu	Cys	Ile	Thr	Gln	Gly	Arg	Val	Leu	Glu	Arg	Pro	Arg	Val	Cys	785	790	795

Pro Lys Glu Val Tyr Asp Val Met Leu Gly Cys Trp Gln Arg Glu  
800 805 810

Pro Gln Gln Arg Leu Asn Ile Lys Glu Ile Tyr Lys Ile Leu His  
815 820 825

Ala Leu Gly Lys Ala Thr Pro Ile Tyr Leu Asp Ile Leu Gly  
830 835 839

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1858 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGATCCGCGT CGGAGATGGA TGTCTCTCTT TGCCCAGCCA AGTGTAGTTT 50  
CTGGCGGATT TTCTTGCTGG GAAGCGTCTG GCTGGACTAT GTGGGCTCCG 100  
TGCTGGCTTG CCCTGCAAAT TGTGTCTGCA GCAAGACTGA GATCAATTGC 150  
CGGCGGCCGG ACGATGGGAA CCTCTTCCCC CTCCTGGAAG GGCAGGATTC 200  
AGGGAACAGC AATGGGAACG CCAATATCAA CATCACGGAC ATCTCAAGGA 250  
ATATCACTTC CATAACATA GAGAACTGGC GCAGTCTTCA CACGCTCAAC 300  
GCCGTGGACA TGGAGCTCTA CACCGGACTT CAAAAGCTGA CCATCAAGAA 350  
CTCAGGACTT CGGAGCATTC AGCCCAGAGC CTTTGCCAAG AACCCCCATT 400  
TGCGTTATAT AAACCTGTCA AGTAACCGGC TCACCACACT CTCGTGGCAG 450  
CTCTTCCAGA CGCTGAGTCT TCGGGAATTG CAGTTGGAGC AGAACTTTTT 500  
CAACTGCAGC TGTGACATCC GCTGGATGCA GCTCTGGCAG GAGCAGGGGG 550  
AGGCCAAGCT CAACAGCCAG AACCTCTACT GCATCAATGC TGATGGCTCC 600  
CAGCTTCCTC TCTTCCGCAT GAACATCAGT CAGTGTGACC TTCCTGAGAT 650  
CAGCGTGAGC CACGTCAACC TGACCGTACG AGAGGGTGAC AATGCTGTTA 700  
TCACTTGCAA TGGCTCTGGA TCACCCCTTC CTGATGTGGA CTGGATAGTC 750  
ACTGGGCTGC AGTCCATCAA CACTCACCAG ACCAATCTGA ACTGGACCAA 800  
TGTTCAATGCC ATCAACTTGA CGCTGGTGAA TGTGACGAGT GAGGACAATG 850  
GCTTCACCCT GACGTGCATT GCAGAGAACG TGGTGGGCAT GAGCAATGCC 900  
AGTGTTGCCC TCACTGTCTA CTATCCCCCA CGTGTGGTGA GCCTGGAGGA 950



GCCTGAGCTG CGCCTGGAGC ACTGCATCGA GTTTGTGGTG CGTGGCAACC 1000  
 CCCCACCAAC GCTGCACTGG CTGCACAATG GGCAGCCTCT GCGGGAGTCC 1050  
 AAGATCATCC ATGTGGAATA CTACCAAGAG GGAGAGATTT CCGAGGGCTG 1100  
 CCTGCTCTTC AACAAAGCCCA CCCACTACAA CAATGGCAAC TATACCCTCA 1150  
 TTGCCAAAAA CCCACTGGGC ACAGCCAACC AGACCATCAA TGGCCACTTC 1200  
 CTCAAGGAGC CCTTTCCAGA GAGCACGGAT AACTTTATCT TGTTTGACGA 1250  
 AGTGAGTCCC ACACCTCCTA TCACTGTGAC CCACAAACCA GAAGAAGACA 1300  
 CTTTTGGGGT ATCCATAGCA GTTGGACTTG CTGCTTTTGC CTGTGTCCTG 1350  
 TTGGTGGTTC TCTTCGTCAT GATCAACAAA TATGGTCGAC GGTCCAAATT 1400  
 TGGAATGAAG GGTCCCGTGG CTGTCATCAG TGGTGAGGAG GACTCAGCCA 1450  
 GCCCACTGCA CCACATCAAC CACGGCATCA CCACGCCCTC GTCACTGGAT 1500  
 GCCGGGCCCCG ACACTGTGGT CATTGGCATG ACTCGCATCC CTGTCATTGA 1550  
 GAACCCCCAG TACTTCCGTC AGGGACACAA CTGCCACAAG CCGGACACGT 1600  
 GGGTCTTTTC AAACATAGAC AATCATGGGA TATTAAACTT GAAGGACAAT 1650  
 AGAGATCATC TAGTCCCATC AACTCACTAT ATATATGAGG AACCTGAGGT 1700  
 CCAGAGTGGG GAAGTGTCTT ACCCAAGGTC ACATGGTTTC AGAGAAATTA 1750  
 TGTTGAATCC AATAAGCCTT CCCGGACATT CCAAGCCTCT TAACCATGGC 1800  
 ATCTATGTTG AGGATGTCAA TGTTTATTTT AGCAAAGGAC GTCATGGCCT 1850  
 TTAAAAAC 1858

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 612 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met	Asp	Val	Ser	Leu	Cys	Pro	Ala	Lys	Cys	Ser	Phe	Trp	Arg	Ile
1				5				10						15
Phe	Leu	Leu	Gly	Ser	Val	Trp	Leu	Asp	Tyr	Val	Gly	Ser	Val	Leu
			20					25						30
Ala	Cys	Pro	Ala	Asn	Cys	Val	Cys	Ser	Lys	Thr	Glu	Ile	Asn	Cys
			35					40						45



Pro	Thr	Leu	His	Trp	Leu	His	Asn	Gly	Gln	Pro	Leu	Arg	Glu	Ser	335	340	345
Lys	Ile	Ile	His	Val	Glu	Tyr	Tyr	Gln	Glu	Gly	Glu	Ile	Ser	Glu	350	355	360
Gly	Cys	Leu	Leu	Phe	Asn	Lys	Pro	Thr	His	Tyr	Asn	Asn	Gly	Asn	365	370	375
Tyr	Thr	Leu	Ile	Ala	Lys	Asn	Pro	Leu	Gly	Thr	Ala	Asn	Gln	Thr	380	385	390
Ile	Asn	Gly	His	Phe	Leu	Lys	Glu	Pro	Phe	Pro	Glu	Ser	Thr	Asp	395	400	405
Asn	Phe	Ile	Leu	Phe	Asp	Glu	Val	Ser	Pro	Thr	Pro	Pro	Ile	Thr	410	415	420
Val	Thr	His	Lys	Pro	Glu	Glu	Asp	Thr	Phe	Gly	Val	Ser	Ile	Ala	425	430	435
Val	Gly	Leu	Ala	Ala	Phe	Ala	Cys	Val	Leu	Leu	Val	Val	Leu	Phe	440	445	450
Val	Met	Ile	Asn	Lys	Tyr	Gly	Arg	Arg	Ser	Lys	Phe	Gly	Met	Lys	455	460	465
Gly	Pro	Val	Ala	Val	Ile	Ser	Gly	Glu	Glu	Asp	Ser	Ala	Ser	Pro	470	475	480
Leu	His	His	Ile	Asn	His	Gly	Ile	Thr	Thr	Pro	Ser	Ser	Leu	Asp	485	490	495
Ala	Gly	Pro	Asp	Thr	Val	Val	Ile	Gly	Met	Thr	Arg	Ile	Pro	Val	500	505	510
Ile	Glu	Asn	Pro	Gln	Tyr	Phe	Arg	Gln	Gly	His	Asn	Cys	His	Lys	515	520	525
Pro	Asp	Thr	Trp	Val	Phe	Ser	Asn	Ile	Asp	Asn	His	Gly	Ile	Leu	530	535	540
Asn	Leu	Lys	Asp	Asn	Arg	Asp	His	Leu	Val	Pro	Ser	Thr	His	Tyr	545	550	555
Ile	Tyr	Glu	Glu	Pro	Glu	Val	Gln	Ser	Gly	Glu	Val	Ser	Tyr	Pro	560	565	570
Arg	Ser	His	Gly	Phe	Arg	Glu	Ile	Met	Leu	Asn	Pro	Ile	Ser	Leu	575	580	585
Pro	Gly	His	Ser	Lys	Pro	Leu	Asn	His	Gly	Ile	Tyr	Val	Glu	Asp	590	595	600
Val	Asn	Val	Tyr	Phe	Ser	Lys	Gly	Arg	His	Gly	Phe				605	610	612

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 790 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met	Leu	Arg	Gly	Gly	Arg	Arg	Gly	Gln	Leu	Gly	Trp	His	Ser	Trp	1	5	10	15
Ala	Ala	Gly	Pro	Gly	Ser	Leu	Leu	Ala	Trp	Leu	Ile	Leu	Ala	Ser	20	25	30	
Ala	Gly	Ala	Ala	Pro	Cys	Pro	Asp	Ala	Cys	Cys	Pro	His	Gly	Ser	35	40	45	
Ser	Gly	Leu	Arg	Cys	Thr	Arg	Asp	Gly	Ala	Leu	Asp	Ser	Leu	His	50	55	60	
His	Leu	Pro	Gly	Ala	Glu	Asn	Leu	Thr	Glu	Leu	Tyr	Ile	Glu	Asn	65	70	75	
Gln	Gln	His	Leu	Gln	His	Leu	Glu	Leu	Arg	Asp	Leu	Arg	Gly	Leu	80	85	90	
Gly	Glu	Leu	Arg	Asn	Leu	Thr	Ile	Val	Lys	Ser	Gly	Leu	Arg	Phe	95	100	105	
Val	Ala	Pro	Asp	Ala	Phe	His	Phe	Thr	Pro	Arg	Leu	Ser	Arg	Leu	110	115	120	
Asn	Leu	Ser	Phe	Asn	Ala	Leu	Glu	Ser	Leu	Ser	Trp	Lys	Thr	Val	125	130	135	
Gln	Gly	Leu	Ser	Leu	Gln	Glu	Leu	Val	Leu	Ser	Gly	Asn	Pro	Leu	140	145	150	
His	Cys	Ser	Cys	Ala	Leu	Arg	Trp	Leu	Gln	Arg	Trp	Glu	Glu	Glu	155	160	165	
Gly	Leu	Gly	Gly	Val	Pro	Glu	Gln	Lys	Leu	Gln	Cys	His	Gly	Gln	170	175	180	
Gly	Pro	Leu	Ala	His	Met	Pro	Asn	Ala	Ser	Cys	Gly	Val	Pro	Thr	185	190	195	
Leu	Lys	Val	Gln	Val	Pro	Asn	Ala	Ser	Val	Asp	Val	Gly	Asp	Asp	200	205	210	
Val	Leu	Leu	Arg	Cys	Gln	Val	Glu	Gly	Arg	Gly	Leu	Glu	Gln	Ala	215	220	225	
Gly	Trp	Ile	Leu	Thr	Glu	Leu	Glu	Gln	Ser	Ala	Thr	Val	Met	Lys	230	235	240	



Leu	Leu	Pro	Glu	Gln	Asp	Lys	Met	Leu	Val	Ala	Val	Lys	Ala	Leu	530	535	540
Lys	Glu	Ala	Ser	Glu	Ser	Ala	Arg	Gln	Asp	Phe	Gln	Arg	Glu	Ala	545	550	555
Glu	Leu	Leu	Thr	Met	Leu	Gln	His	Gln	His	Ile	Val	Arg	Phe	Phe	560	565	570
Gly	Val	Cys	Thr	Glu	Gly	Arg	Pro	Leu	Leu	Met	Val	Phe	Glu	Tyr	575	580	585
Met	Arg	His	Gly	Asp	Leu	Asn	Arg	Phe	Leu	Arg	Ser	His	Gly	Pro	590	595	600
Asp	Ala	Lys	Leu	Leu	Ala	Gly	Gly	Glu	Asp	Val	Ala	Pro	Gly	Pro	605	610	615
Leu	Gly	Leu	Gly	Gln	Leu	Leu	Ala	Val	Ala	Ser	Gln	Val	Ala	Ala	620	625	630
Gly	Met	Val	Tyr	Leu	Ala	Gly	Leu	His	Phe	Val	His	Arg	Asp	Leu	635	640	645
Ala	Thr	Arg	Asn	Cys	Leu	Val	Gly	Gln	Gly	Leu	Val	Val	Lys	Ile	650	655	660
Gly	Asp	Phe	Gly	Met	Ser	Arg	Asp	Ile	Tyr	Ser	Thr	Asp	Tyr	Tyr	665	670	675
Arg	Val	Gly	Gly	Arg	Thr	Met	Leu	Pro	Ile	Arg	Trp	Met	Pro	Pro	680	685	690
Glu	Ser	Ile	Leu	Tyr	Arg	Lys	Phe	Thr	Thr	Glu	Ser	Asp	Val	Trp	695	700	705
Ser	Phe	Gly	Val	Val	Leu	Trp	Glu	Ile	Phe	Thr	Tyr	Gly	Lys	Gln	710	715	720
Pro	Trp	Tyr	Gln	Leu	Ser	Asn	Thr	Glu	Ala	Ile	Asp	Cys	Ile	Thr	725	730	735
Gln	Gly	Arg	Glu	Leu	Glu	Arg	Pro	Arg	Ala	Cys	Pro	Pro	Glu	Val	740	745	750
Tyr	Ala	Ile	Met	Arg	Gly	Cys	Trp	Gln	Arg	Glu	Pro	Gln	Gln	Arg	755	760	765
His	Ser	Ile	Lys	Asp	Val	His	Ala	Arg	Leu	Gln	Ala	Leu	Ala	Gln	770	775	780
Ala	Pro	Pro	Val	Tyr	Leu	Asp	Val	Leu	Gly						785	790	

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TGYGAYATHA TGTGGYTNAAC 23

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TGGATGCARY TNTGGCARCA RCA 23

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

YTCRTCYYTN CCRTAYTCRT T 21

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CCYTCYTGRY ARTAYTCNAC GTG 23

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CACGTCAACA ACGGCAACTA CA 22

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GGAAGGATGA GAAACAGATT TCTGC 25

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CATCAATGGC CACTTCCTCA AGG 23

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

AGGTGTTTCG TCCTTCTTCT CC 22

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GAGATGTGCC CGACCGGTTG TATC 24



(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CACAGTGATA GGAGGTGTGG GA 22

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGATGTGGCT CCAGGCCCC 19

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GGGCAACCCG CCCACGGAA 19

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ACGCCAGGCC AAGGGTGAG 19

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: Nucleic Acid

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TAACCACTCC CAGCCCCTGG 20

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TTGGTGGCCT CCAGCGGCAG 20

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

AATTCATGAC CACCAGCCAC CA 22

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GTCCTCGGG ACTGCGATGC 20

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ATGTCGCCCT GGCCGAGGTG GCAT 24

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AAGCTCAACA GCCAGAACCT C 21

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CAGCTCTGTG AGGATCCAGC C 21

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CCGACCGGTT TTATCAGTGA C 21

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

ATGATCTTGG ACTCCCGCAG AGG 23

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CTTGGCCAAG GCATCTCCGG T 21

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

ATGTGCAGCA CATTAAGAGG A 21

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

TTATACACAG GCTTAAGCCA TCCA 24

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

AGGAGGCATC CAGCGAATG 19

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 9 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Glu Ser Thr Asp Asn Phe Ile Leu Phe  
1 5 9

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Leu Phe Asn Pro Ser Gly Asn Asp Phe Cys Ile Trp Cys Glu  
1 5 10 14

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TCTCCTTCTC GCCGGTGG 18

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 6 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Ser Pro Ser Arg Arg Trp  
1 5 6

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Phe Val Leu Phe His Lys Ile Pro Leu Asp Gly  
1 5 10 11

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 84 amino acids  
 (B) TYPE: Amino Acid  
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Trp	Val	Phe	Ser	Asn	Ile	Asp	Asn	His	Gly	Ile	Leu	Asn	Leu	Lys
1				5					10					15
Asp	Asn	Arg	Asp	His	Leu	Val	Pro	Ser	Thr	His	Tyr	Ile	Tyr	Glu
				20					25					30
Glu	Pro	Glu	Val	Gln	Ser	Gly	Glu	Val	Ser	Tyr	Pro	Arg	Ser	His
				35					40					45
Gly	Phe	Arg	Glu	Ile	Met	Leu	Asn	Pro	Ile	Ser	Leu	Pro	Gly	His
				50					55					60
Ser	Lys	Pro	Leu	Asn	His	Gly	Ile	Tyr	Val	Glu	Asp	Val	Asn	Val
				65					70					75
Tyr	Phe	Ser	Lys	Gly	Arg	His	Gly	Phe						
				80				84						

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